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FEATURES
      SOURCE
      location/Qualifiers
      1..670
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone_lib="BN0034"
      /dev_stage="Adult"
      /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
      Site_2: SmaI; A mini-library was made by cloning products
      derived from ORESTES PCR (U.S. Letters Patent application
      No. 196,716 - Ludwig Institute for Cancer Research)
      profiles into the pUC 18 vector. Reverse transcription of
      tissue mRNA and cDNA amplification were performed under
      low stringency conditions."
BASE COUNT
227 a 105 c 164 g 170 t
ORIGIN

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Query Match	39.6%;	Score 612;	DB 11;	Length 670;
Best Local Similarity	97.3%;	Pred. No. 1.9e-139;		
Matches 644;	Conservative 0;	Mismatches 15;	Indels 3;	Gaps 2

QY	188	cagtaataagaaacagaagacccaaagccaaacatttaatacaatgtctccaa	247
Db	4	CTGTACATGAAACAGAACGC--AAAGCCAAACAATTATACATGTCTCAATGG	61
QY	248	actacttctaagggaaaacatttcattgtatatactccagaagaaaggaaatgaca	307
Db	62	ACTTACTTTATAGAGACACATTTTCATGTATGATCTCCAAAGCAAAAGGAATGCACA	129
QY	308	gaagctatccaaggtctgtagacagacagctcagagcgcaagaagaggaatgaaatgct	367
Db	122	GAACCTATCCAGCGCTGTAGCAGACAGACTGCAGAGCCACAAGAGAGGAAATGAATTGT	181
QY	368	agttccacttcacaatatgtataataatagggaggaagaaagatgcatgccttacaacccat	427
Db	182	AGTCCAACTTCACAAATGTATATATGAGAGAGCAAGATGTGCTCTTACAAACCCAT	241
QY	428	catataaagaagaacaatgaaatgattttgactattgaaactaagtaagacacttt	487
Db	242	CATTAAGAAGAAACATATGATGATTTTGACTATTTCGAAACTACTAGGTAAAGCACTTTG	301
QY	488	gggaagaattatctgtgtctgagagaagcaagctgg--aaaaatactatgctaagaaattct	546
Db	302	GGGAAATGTTTGTGGGTTCGAGAGAAGGCAAGTGGAATAATFACATGTATGAAGATTCT	361
QY	547	gaagaaagaagtcaattatctcaagaatgaaatgagcaaaccttaactgaaagcaagt	606
Db	362	GAAGAAAGAAAGTCAATTATTCGAAAGGTGAAGTGAGCACACACTCTAACTGAAGCAAGAGT	421
QY	607	attaaagaacaactagacatccctctttaaactccttgaatatctctccagacaaaga	666
Db	422	ATTAAAGAACACTAGACATCCCTTTTAAATCTCTTGAATATTCTCTCCAGCAAAAGA	481
QY	667	ccgtttgtgtttgtgtatggaataatgtaaaggggcgagctgttcttccattgttcgag	726
Db	482	CCCTTGGTGTTTGATGAAATATGTATATGGGGCGAGCTGTATTTCATTTGTCGAG	541
QY	727	agagcgaggtctctcgaagacccgaacgtttctatgcttgagaaatgtctctgcct	786
Db	542	AGAGCGGTTTCTCTGAGGACCGCACACGTTTCTATATGGTGCAGAAATGGTCTCTCTCTT	601
QY	787	ggaactatcaatctccgaaagaattgttgtaacgttgatctcaagtgtgaaatctaagct	846
Db	602	GGACTATCTACATTCGGAAGAAGATGTGTGGCTGTATCTCAAGTTGGAGATCTAATGCT	661
QY	847	gg 848	
Db	662	GG 663	

LOCUS	BE779151				
DEFINITION	BE779151	876 bp	mRNA	EST	20-OCT-2000
ACCESSION	601466777PFI	NIH_MGC_67	Homo sapiens cDNA clone	IMAGE:3867931	5'
VERSION	BE779151				
KEYWORDS	BE779151.1	GI:10200349			
SOURCE	ESF.				
ORGANISM	human.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
JOURNAL	1 (bases 1 to 876)				
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .				
	National Institutes of Health, Mammalian Gene Collection (MGC).				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgabbs-remail.nih.gov				
	Tissue Procurement: ARCC				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Plate: LMA9615 row: a column: 20				
	High quality sequence start: 6				
	High quality sequence stop: 660.				
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source	1..876				
	Location/Qualifiers				

FEATURES
Source

BE779151 876 bp mRNA
 20-OCT-2000
 601444773F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867531 5',
 mRNA sequence.
 BE779151
 BE779151.1 GI:10200349
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 876)
 NIH-MGC <http://mgc.ncl.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph. D.
 Email: cgabs-r@mail.nih.gov
 Tissue procurement: AMCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLA95615 row: a column: 20
 High quality sequence start: 6
 High quality sequence stop: 660.

BASE COUNT	301 a	163 c	217 g	195 t
/db_xref="taxon:9606" /clone_image="3867931" /clone_1lb="NIH_MGC_67" /tissue_type="retinoblastoma" /lab_host="DH10B (phage resistant)" /note="Organ: eye; Vector: pCMV-SORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Library constructed by Life Technologies."				

Query Match	33.8%	Score	523.4	DB	10	Length	876
Best Local Similarity	89.4%	Pred. No.	1e-117				
Matches	691	Conservative	0	Mismatches	61	Indels	21
						Gaps	11

QY	1	ggaggtcacaatgagcagatgttaccattgttgaagaagatgttgggttcagaagaggggaga	60
Db	17	GGGAGCTATCATGTGCGCATGTTCACATTGTGTGAAGAGTGGTGGTTAGAAAGCGGAGA	76
QY	61	atatataaaaaactcygagggccaagatacttcctctttgaagacagatggtccatctcag	120
Db	77	ATATATAAAAAACGTGGAGGCGCAAGATACCTTCCTTTGAAGACAGATGGCTCATTCATAGG	136
QY	121	atataaagagaaaccttcaagatgttgaatttacccttaccctcaacaacttttcagtgyc	180
Db	137	ATATAAAGAAACCTCAAGATGTGGATTACCTTATCCCTCAACAACCTTTTCAGTGGC	196
QY	181	aaaaatgcagttatatgaaaacagaaagccaaagccaaacacatttaatactagatgct	240
Db	197	AAATGCGCAATTTATGTAAACACAGAACGCCAAAGCCAAACATTTTATATCAGATGTCT	256
QY	241	ccagtggaactcactggttatagagaagaacatttcabtlagatacttcacagaagaaagggaga	300
Db	257	CCAGTGACACTACCTTTATAGAGAGAACATTTCATGTAGATCTCCAGAGAAAGGAGAGA	316
QY	301	atgagacaagaagctatccagagctgttagcagacagactgcagagycagaagaagagagaaat	360
Db	317	ATGGAACAGAAAGCTATCCAGGCTGTACAGACACTGCAAGAGGCAAGAAAGGAGAGAAT	376
QY	361	gaatttgatgccacttcacaaattgataataatagagagagagagatgtgacctctac	420

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Db 377 GAATTGAGTCCAACTTCACAAATGATATATAGAGAGGAAGAGATGATGCTCTTAC 436
Oy 421 aaccatcataaagaagaacaatgaatatttgactatttgaaactctggtaaag 480
Db 437 AA-CCATCATTAAGAAGAAACACATGATGATTTTGACTATTTGAAACTACTAGTAAAG 495
Oy 481 cactcttgggaagtatttggcttcgagaagaagcaagtggaanaa-tactatgctatga 539
Db 496 CACTTT--GGGAAGATTATTTGGTTGAGAGAGAGCAATGGAAAACACTACTATGATATA 553
Oy 540 aga-ttcgagaagaaga-gtcattattgcaagaagatgaatgycacacac---tctaac 594
Db 554 AGATTCTGGAAGAAAGAGAGGTCTATTCATGCAAGATGAACGTGGCACCACTCCTTAC 613
Oy 555 tgaagc---agagtatttaagaacactag---acatcccttcttaactcctt---gaa 645
Db 614 TGAAGAGCCAGAGATTAATTAACAGACACTGACACTTCCCTTTTAAACCTCTTGAA 673
Oy 646 atatccctccaga-caaagacgcttgcttgcttgatggaataatgttaa--tggagg 702
Db 674 TTATTCCTTCCAGACCAGACAGACCCGTACGCTAGCTGATGACTATGTTAATGTGGGC 733
Oy 703 cgagctgtttccattgttcgagaagcggtgtctctctcgtgagaccgcacac 755
Db 734 GAAGCTGATGTGTCATATGTGAGAGACGGGGTCCGAGACGAACAGCTAC 786

RESULT 3
LOCUS AW960221 607 bp mRNA EST 01-JUN-2000
DEFINITION EST372292 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION AW960221
VERSION AW960221.1 GI:8149905
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 607)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,J.R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,Y., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 143
Seq primer: Reverse.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="MAGE resequences, MAGF"
/note="Vector: pBluescriptSkm"
BASE COUNT 221 a 104 c 147 g 135 t
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Best Local Similarity 97.9%; Pred. No. 8e-114;
Matches 514; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Oy 1 gggagtcacatgagcagctgttacatgtgnaaagaaggttgctcagaaggaggaga 60
Db 83 GGGAGTCATCATGAGCGAGTGTACCATGTGTGAAGAAGAGGTGGTTCAAGAGGGGAGA 142
Oy 61 atataaaaaactgagagccaagatacttcttgaagaagaatggtcattcataag 120

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Db 143 ATATATAAAAACTGGAGCCAAAGATACCTCTTTTGAAGACAGATGCTCATTTAGG 202
Oy 121 atataaagaagaacctcaagatgtgatttacttctccccaacttctcagtc 180
Db 203 ATATTAAGAGAAACCTCAAGATGTGATTTACTTATCCCTTCAACACTTTTCACTGCG 262
Oy 181 aaatgccagttaatgaagaacagacgaacgaacccaacacattatatcaagatgct 240
Db 263 AAAATCCAGTTATATATAAACAAGACAGACCAAGCCAAACACATTATATCAGATGCT 322
Oy 241 ccagtgactactgtatatagagaacattcaatgtagatactccagagaaaggaga 300
Db 323 CCAGTGCATAGCTATATATAGAGACATTTTCATATGATCTCCAGAGAAAGGAGAGA 382
Oy 301 atggaagaagctatccagctgtagcagacagacgtcagagggcaagaagaagaat 360
Db 383 ATGACAGAGAGCTATTCAGAGCTGTACACACACACGACAGAGCAAGAGAGAGAA 442
Oy 361 gaattgagtcacactcaaatgataatataagagaagaagaatgagctctac 420
Db 443 GAATTGTATTCACACTTCACAAATTTATATATATAGAGAGAGAGATGATGCTTAC 502
Oy 421 aaccatcataaagaagaacaatgaatatttgactatttgaaactactagtaag 480
Db 503 AACCCATCATTAAGAAGAAACACATGATGATTTTGACTATTTGAAACTACTAGGAAAG 562
Oy 481 cactcttgggaagtatttggcttcgagaagaagcagtgaaa 525
Db 563 CACTTTTGGGAAGTATTTTGGTTGAGAGAAAGCAAGCTGAAA 607

RESULT 4
LOCUS AL548951 1000 bp mRNA EST 16-FEB-2001
DEFINITION AL548951.L1.NFL006.PL2 Homo sapiens cDNA clone CS0D1042YE16 5
prime, mRNA sequence.
ACCESSION AL548951
VERSION AL548951.1 GI:12884464
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1000)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Genoscope - Centre National de Sequencage
BP 191 91006 EVRI cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="CS0D1042YE16"
/clone_lib="L1-NFL006-PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site:1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com url :
http://fulllength.invitrogen.com"
BASE COUNT 219 a 289 c 289 g 189 t 14 others
ORIGIN
Query Match 32.6%; Score 503.8; DB 10; Length 1000;

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Best Local Similarity 71.0%; Pred. No. 6,7e-113;
Matches 709; Conservative 11; Mismatches 268; Indels 11; Gaps 4;

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QY 439 gacaaagaatgatttgactcatttgaaactactagtgaaagacatttgggaagtat 488
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Db 9 GACCAATGAACGAATTTAGTACTGCTGGGCAAGGACCTTTGGCAAGGAT 68
QY 499 ttgtgtcgaagaagaagtgaaatactatgtctataaagattctgaaagaaga 558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 CCGKTKAAGAAAGAGCCAGCCAGCCG-TACTACGCCATTAAGATCTCAAGAGAGT 127
QY 559 cactatgcaagaagtagaagtgacacacacttaactgaagagatlaaagaac 618
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Db 128 CATCGTGGCCAGAGAGAGTGGCCACACACATCACCGAAGACCGCTCTCGAAGATC 187
QY 619 taagacatcccttttaacatccttgaaatattctctccagacaaagaccgttgg 678
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Db 188 CACACACCCCTTCTCTCACACCCCTGAATCTTTCTTCAACACCCACACCGCTCTT 247
QY 679 tgtgatgaaatgtaattgagggagagctgtttccacttgcagagagcggtgtt 738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 248 TTKCATGAGATAGCCCAAGCGGGGCGAGCTTCTTCTTCTTCTTCTTCTTCTTCTT 307
QY 739 ctctgagagacgcacacglttctatgtgcagaatgtctctgaccttgactatca 788
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Db 308 CTCGAGAGACCGGGCGCTTCTATGCTGAGATGTGTGAGCCCTGGACTACCTGCA 367
QY 799 ttccggaaga---ttgtgacgltgatacctgaagtgagaatcgaatgctggaaga 855
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QY 856 tggccacataaaaaattacagatttggacttgcagaagaaggatcacagatgcagcac 915
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QY 916 catgaagaactctgtggaactccagaatactgcgaacagagtggttagaagata 975
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Db 488 CATKAGACCTTTGGGGCACACCTGAGTACCTGGGCCCGGAGGTGTGAGAGACATGA 547
QY 976 ctatgcccgaagtagaagtggtgagggcctgaagggtgtgcatatgataatgtgtg 1035
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Db 548 CTACGGCGCTGACAGTGTGAGTGGGGGCTGGGCGTGTGTATGACAGATGATGTGG 607
QY 1036 gaagttacatttctacacacagagacatgagaacttcttgaaataataatgaga 1095
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Db 608 TCGCGTGGCTTCTACACACAGAGACCATGGAAGCTTTTGAGCTCATCTCATGAGGA 667
QY 1096 cattaattctctgaacac-tctctcagaatgcaaaatcatgtcttcaaggctctga 1154
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Db 668 GATCCGCTTCCCGCACGCTTGGGTCCCGAGGCCAAGTCTTTCAGGGCTGCTCA 727
QY 1155 taagaagacaaataaagccttggtgagagacagatggtgcagaagaataatgagac 1214
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QY 1215 acagttctctctctgagtaactggaagatgtatatagtlaaaagctgttaccctt 1274
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Db 848 TCAAGCCCCAGTACAGTGTGAGACACAGTATTTGATGAGAGATTCACGGCCC 907
QY 1335 agactcttaacaataaacaacacgtaaaataatatagtatgagtgatgactgacatgaca 1394
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Db 908 AGATGTATCATCATACACACACGACCAA-----GATGACACAGATGAGTGTGTGACA 961
QY 1395 atgaagagcgccgacttccctcaatttccactctg 1433
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RESULT 5

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LOCUS AL545564 1027 bp mRNA EST 16-FEB-2001
DEFINITION AL545564.LRI.NFL006.PL2 Homo sapiens cDNA clone CS0D1015Y11.5
ACCESSION AL345564
VERSION AL545564.1 GI:12878046
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1027)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLES Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/issue_type="Placenta"
/notes="Vector: PCWVSPORT 6; Site: 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/
BASE COUNT 223 a 293 c 320 g 188 t 3 others
ORIGIN
Query Match 32.4%; Score 502; DB 10; Length 1027;
Best Local Similarity 70.7%; Pred. No. 1.8e-112;
Matches 724; Conservative 1; Mismatches 291; Indels 8; Gaps 4;
QY 227 ataataagatgtctcagtgactcgtgtatagagaacatttgaatgatactca 286
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Db 2 ATATCCGCTGCTCGAGTGAGACACTGTATGAAGCACCTTTCATGTGGAGACTCT 61
QY 287 gaagaaaggaagaatgagacagaagctatccagctgttagacagacagactgcagagcaa 346
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Db 62 GAGGAGCGGAGAGAGTGAAGACCAACCCATCAACACTGTGCTGACGGCTCAAGAGCAG 121
QY 347 gaagaggaagaatgaatgttagtccaaacttccaaatgtataataatagaagaagag 406
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Db 122 GAGGAGAGAGAGATGACTTCCGTCGGGCTCAACCCAGTGCACAACTCAGGGCTGAAGAG 181
QY 407 atgagtgccctcaaacaccatc---ataaagaagaagaatgaatgaatgttgaacttg 463
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Db 182 ATGAGAGTGTCCCTGGCCAAAGCCCAAGACACCGGCTGACATGAACGATTTGATGACT 241
QY 464 aaactaagtaglaaagcacttctggaaagtatttggltctggaagaagaagatgaga 523
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Db 242 AAGCTCTGGCGCAAGGGCACTTTGGCGAAGGTATCTGTGTGAAGGAAGGCGCACAGGC 301
QY 524 aaactatagtctatgaagatctgaaagaagaatcaattatgtgcaagaagtagagca 583
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Db 302 CGCTACTAGCCCATGAAGATCTCTCAAGAGGAAGTATGCTGTGCAAGGACGAGTGGCC 361
QY 584 cacacttaactgaagaagagatataaagaacacatgacatccctttaaactcttg 643
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Db 362 CACACATCATCGAAGACCGCTCTGACGAATTCACAGGACCCCTTCTCTCAGAGCCCTG 421
QY 644 aaatattcctccagacaaagacgltgtgtgttctgtatgtaatgtlaatgagggc 703
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QY 1073 ttgtaataataataatggaaga 1095
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Db 842 TTTGAGCTCATCTCATGAGGA 864

RESULT 7
LOCUS BG686874 948 bp mRNA EST 01-MAY-2001
DEFINITION 602650859F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763151 5',
mRNA sequence.
ACCESSION BG686874
VERSION BG686874.1 GI:13918271
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS NIH-MGC <http://mgi.mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1618 row: f column: 16
High quality sequence stop: 932.

FEATURES
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/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 217 a 274 c 292 g 165 t
ORIGIN

Query Match 28.3%; Score 437.8; DB 11; Length 948;
Best Local Similarity 70.1%; Pred. No. 9, 7e-97;
Matches 660; Conservative 0; Mismatches 272; Indels 9; Gaps 5;

QY 5 gtcacatgagatgttccattgtgaagaaggttggttgaagaaggaggagatat 64
|||||
Db 2 GGCACCATGAGCGACGTGCTATTGTGAAGAGAGGTTGGCTGCACAAAGAGGAGGTAC 61

QY 65 ataaaaaacttgagagcagaatctctcttgaagaagaatgagtcattcatagatat 124
|||||
Db 62 ATCAAGACCTGGCGGCGCACGCTACTCTCTCAAGAAATGATGGCACCTTCATTGGCTAC 121

QY 125 aaagaanaactcaagaatgttgatctta---tccctcaacaactttcaagtga 181
|||||
Db 122 AAGGACGGCGCGGAGATGTGGACCAAGCGAGGCTCCCTCAACAACACTTCTGTGGGG 181

QY 182 aaatgcagtttaataaagaagaagcaagaagcaacaatttaataatcagatctc 241
|||||
Db 182 CAGTGCACGCTGATGAAGAGGAGCGGCCGCCACACACCTTCATCATCCGCTGCTG 241

QY 242 cagtggaactgttataagaagaacatttcatgtatgatactccagaaggaagaaga 301
|||||
Db 242 CAGTGGACGACCTGTCATTCAGAACGACACCTTCATGTGAGAGCTCTGAGAGGAGGAG 301

QY 302 tggacagaagctatccaagctgttagcagacagacgtcgaagaggaagaagaatg 361
|||||
Db 302 TGGACAACCGCCCATCCAGACTGTGGCTGAGCGGCTCAAGAACGAGAGGAGGAGATG 361

QY 362 aattgtatgtccaacttcacaattgataatataatggaagaagaatgtgacttaca 421
|||||
Db 362 GACTTCGGTTCGGCTCACCACTGACACTCAGGGGCTGAAGAGATGGAGGTGTCCTTG 421

QY 422 acccatc---ataaagaagaagaatgaatgtatgttgaatttgaactactaggtaaa 478
|||||
Db 422 GCCAAGCCCAAGACACCGCGTACCATTAAGCAAGATTTGAGTGAAGCTGCTGGGCAAG 481

QY 479 ggcacttttgggaagttatgttgcgcgaagaaggaagtgaaataactatgtatg 538
|||||
Db 482 GGCACCTTTCGGCAAGGTGATCTGTGAAGGAGAAAGCCACAGCGCGCTACTACGCCATG 541

QY 539 aagattctgaagaagaagcatattgtgaagaagatggaagtgacacactcaactgaa 598
|||||
Db 542 AAGATCCTCAAGAGAGATCATCTGTGCCAAGACGAGGTGGC-CACACACTCACCGAG 600

QY 599 agcagatataaagaacacttagacatccctttaaactccttgaataatcctccag 658
|||||
Db 601 AACCGGCTCCTGAGAACTCAGACACCCCTTCTCAGACCCCTGAAGTACTTTTCAG 660

QY 659 acaaaagaccgtttgtttgttgcgtgaatgttaatgtggggcgagctgtttccat 718
|||||
Db 661 ACCCAGACCGGCTCTGTCTTGTTCATGAGTACGCCAAGCGGCGGAGGCTGTCTTCAC 720

QY 719 ttgtcgaagagcgggtgttcttctgagagccgacacglttcatgtgcagaatt-gt 777
|||||
Db 721 CTGTCCCGGAGCGGTGTGTTCTCCGAGGACGGGCGGCTCTATGCGCTGAGATTGGT 780

QY 778 ctctgcttggaaatcct-acattccggaagaatgttgaacgttgatcgaattgga 836
|||||
Db 781 GTACGCGCTGTGACTACTGACTGAGAGAACAGCTGTGTACCGGACCTCAAGCTGAGA 840

QY 837 atctaagtctgcaagaatggtgcacataaaataacagaatttggacttgcagaag 896
|||||
Db 841 ACCTCATGCTGACGACGAGCGGACACATTAAAGATCAACACTTCGGGCTGTCCAGAGG 900

QY 897 ggtacagatgacgcaccatgaagaacattctgtgacct 937
|||||
Db 901 GGATCCAGGCGCGGTGCCACCATGAATAACTTTGGGGCACACT 941

RESULT 8
AL600183 444 bp mRNA EST 14-AUG-2001
LOCUS DKFZP313J0132_r1 313 (synonym: h1cc2) Homo sapiens cDNA clone
DEFINITION DKFZP313J0132 5', mRNA sequence.
ACCESSION AL600183
VERSION AL600183.1 GI:15163689
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS Bloecker, H., Boecker, M., Brandt, P., Mewes, W., Well, B. and Wiemann, S.
TITLE (Bloecker, H., Boecker, M., Brandt, P., Mewes, H.W., Well, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT MIPs
Am Klopfersplitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

QY	863	atataaatcaagatttggagcttgcacaaagaagagatcaacagtcagcagccaccttgag	922
Db	541	ATTAAATCACAGACTTGGGCGCTGTGTCAGAAAGAGGGGATCAAGAGCGTGTCCACCATGAG	600
QY	923	acattctgtygcactccagaatatctggcaccagaagtgtytgaagaataactatgac	982
Db	601	ACCTTTTTCGGGCACACCTGAGTACCTGGCCCCCGAGAGTGCAGACAAATGACTACGAGC	660
QY	983	cgagagcagtagactgtgtagggcgcttaagggtttgtcagtatgtgaatatgtg-tggagagtt	1041
Db	661	CGTCGAGTGTGACTGTGGGGGGCTGGGCGCTGTGTCATGTACGAATGATGTGCCGGTGCCT	720
QY	1042	acccttctcaacaccagccacatgagaaacttttgaataataataatgaagacatlaa	1101
Db	721	GCCCTTTCACAAAGCAGAGACATGACAGACCTTTTGTAGCTCATCTCATGAGAGAGA-TGC	779
QY	1102	attctctggaacacctcttccaatgacaaatcatctgttccaaggcccttgataaaga	1161
Db	780	GTTCCCGGCACACGCTTGCTGCGAGGCCAAGTCTTGTTCAGGGGCTGCTCAGAGAGG	839
QY	1162	tcc	1164
Db	840	ACC	842
RESULT	10		
LOCUS	BG913158		
DEFINITION	BG913158	749 bp mRNA	EST
ACCESSION	602811788r1	NCI_CGAP_Brn67	Homo sapiens CDNA clone IMAGE:4943877
VERSION	BG913158		
KEYWORDS	BG913158.1	GI:14293634	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
JOURNAL	1 (bases 1 to 749)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabps-remail.nih.gov Tissue Procurement: David N. Louis, M.D. CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLW at: http://image.lnl.gov Plate: LHAM10887 row: p column: 22 High quality sequence stop: 747. Location/Qualifiers 1..749 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4943877" /clone_id="NCI_CGAP_Brn67" /tissue_type="anaplastic oligodendroglioma with 1p/19q loss" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: brain; Vector: PCMV-SpORt6; Site: 1; Notf: Site_2: Salt; Cloned unidirectionally. Primer: Oligo dT Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." 159 a 219 c 228 g 143 t		

Query Match	26.4%	Score 408.2;	DB 11;	Length 749;
Best Local Similarity	72.5%;	Pred. No. 1.7e-89;		
Matches 543; Conservative	0;	Mismatches 203;	Indels 3;	Gaps 1.

OY	515	ggaugtvgaaataactatctatctgtatgtaagatcttcgaaagaagaagctatattctgcaagagt	574
Db	1	gccacagggcgcttactacaccccatgaaagatcttcaagaagaaagctatcttgcgcaaggac	60
OY	575	gaagtcgacacacactctaacctgaagccagatataaagaacactgaaatccctttta	634
Db	61	gaggtggtcccaacactaccgaagaaacccgcttctgcagaactccagagaccccttctc	120
OY	635	acalccttgaataatctccttcacagcaaaagacscgtttgttttgtatgtaatatgt	694
Db	121	acagcccttgaaatactcttccagacacccacgacccgcttgcgtttgtcatgagatgcgcc	180
OY	695	aatggggggagacgtttttccatttgcctgaaagagcggtgttctctgaagaccgcaaa	754
Db	181	aacgggggggacactgtttcttccacctgtcccggaacggtgttctccagagaccgggcc	240
OY	755	cgcttctatgctgcagaataatgttctctgtccttggaactatctacatccgaaaga---	811
Db	241	cccttctatgctgcgcttgagattttgtacgccccttgagacttaccttcgagaaagacgtg	300
OY	812	gtgtacscgtatcctcaagtttggagaatctaaatgctcgtgacaaagatgacaaataa	871
Db	301	gtgtacccgggacctcaagctggagaaacctcatgtcgacacagagcgggacacatttaagatc	360
OY	872	acagatatttggacatttgcagaagaagygatcaagatgcagccacatgaagacattcvt	931
Db	361	acagacttccgggctctgcgaagggggaatcaaggacgggtccaccatgaaagaccttcttgc	420
OY	932	ggcactccagaatactctgacacagagtggttagaagaataatgactatgcccagacgt	991
Db	421	ggcacaacctgaaataccttgcccccccaagtgcttggaagacaaatgactacggcctgtcacgtg	480
OY	992	gaactgtggggccttagggggttgtcatgtatgtaatgatatgtggtggaggttaccttctac	1051
Db	481	gactgtgggggctggggcgtggtcatgtgacagatgatgtgctgggctgcctcttctac	540
OY	1052	aaccagagacatgaaaaacttttgaatataataataatgaagaaacataaatttccctga	1111
Db	541	aaccagagacatgaaagaggttttttagcctacatctcattgagagagatgcgttcccgccc	600
OY	1112	acaactctcttaagatgcaaaaactatctgtccttcaaggcctctgtataaagaatccaataaa	1171
Db	601	acgcttgggttcccgagagccaaagcttcttgccttttagggcttctctaagaaagaccccaagcg	660
OY	1172	cgactctgtgtgagacccaatgatatgcaaaagaataatgagacacagttcttctctgga	1231
Db	661	agcgttgggggggctccgagagacccaagagatcatgcacacatgcgttcttggcgggt	720
OY	1232	gtaaacctggcaagatgtatatataaaaa	1260
Db	721	atcgtgtggcagcacgctgtacgaagaa	749

RESULT	11
TITLE	AA479072/c
LOCUS	
DEFINITION	AAA79072 403 bp mRNA EST 08-AUG-1997 zvl17607.sl Soares_hnpmlp.sl Homo sapiens cDNA clone IMAGE:753876 3 similar to gb:M63167 RAC-ALPHA SERINE/THREONINE KINASE (HUMAN);;
ACCSSION	MRAA sequence.
VERSION	AA479072
EYWORDS	EST. human.
ORGANISM	Homo sapiens
SOURCE	Karyotype; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 403)
AUTHORS	Hillier,L., Allen,M., Bowles,L., Dubouq,T., Getsef,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Matra,M., Mattin,J., Moore,B, , Schellenberg,K., Stepien,W., Tan,F., Theising,B., White,Y., Wylie, , T., Waterston,R. and Wilson,R.
JOURNAL	WashU-Merck Est Project 1997 unpublished (1997)

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 370.

FEATURES

source

1. 403
/organism="Homo sapiens"
/db_xref="GDB:5976747"
/db_xref="taxon:9606"
/clone="IMAGE:753876"
/clone_11b="Soares-NbHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2bHMP, pregnant uterus
NbHMP, and fetal heart NbHMP19) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 87 a 94 c 69 g 153 t
ORIGIN

Query Match 26.1%; Score 403; DB 10; Length 403;
Best Local Similarity 100.0%; Pred. No. 2.8e-88;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 gTgaagaaggttggttcagaagaagggagaataataaaaaactgtgagccaaagatc 88
DB 403 GTGAAGAAGGTGTTGGTTCAGAAAGGAGGAGAAATATATATAAAACTGAGGCCAAGATAC 344
OY 89 ttcccttgaagaagagatggtcattcatagatatataaagaagaacctcaagatgagat 148
DB 343 TTCCCTTTGAAGACAGATGCTCATTCATAGATATATAAGAGAAACCTCAAGATGAGAT 284
OY 149 ttacctatccctcaaacactttcagtgagcaaaatgccaagtttaagaaacaaga 208
DB 283 TTACCTTATCCCTCAACAACCTTTTCAGTGGCAAAATGCCAGTTATGAAACAGAACGA 224
OY 209 ccaagccaaacacatttaacagatgtctccagtgagactactgtlataagagaaga 268
DB 223 CCAAGCCAAACACATTATATCATGATGCTCCAGTGACGACTGTATAGAGAACAA 164
OY 269 ttccatgtatgatactccagaagaagggagaagatgtgacgaagactcaagctgtaga 328
DB 163 TTTTCATGTAATGATCTCCAGAGAAAGGAAGATGACAGAAAGCTATCCAGGCTGTAGCA 104
OY 329 gacagactgcagagcaagaagaagagagaaatgaattgaatgagccaactcacaaattgat 388
DB 103 GACAGACTGCAGAGCCAGAGAAAGAGAGAAATGAATTTGATGTCCAACTTCACAAATTGAT 44
OY 389 aatataagagaagaagatgtgactccttacaaccatcata 431
DB 43 AATATAGAGAGAGAGATGATGCTCTACAAACCATCATA 1

RESULT 12
LOCUS BG775183 1127 bp mRNA EST 15-MAY-2001
DEFINITION 602650376F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:4761259 5',
mRNA sequence.

ACCESSION BG775183
VERSION BG775183.1 GI:14045500
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1127)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTP/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LNCMI613 row: g column: 20
High quality sequence stop: 770.

FEATURES

1. 1127
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4761259"
/clone_11b="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming,
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCCACAG(c). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT 253 a 336 c 330 g 208 t
ORIGIN

Query Match 25.6%; Score 395.6; DB 11; Length 1127;
Best Local Similarity 71.2%; Pred. No. 2.2e-86;
Matches 594; Conservative 0; Mismatches 229; Indels 11; Gaps 5;

OY 527 tactatgcatgaagatctctgaagaagaagatcatattgtcaagaagatgaatgagacac 586
DB 7 TACTAGCCATGAAGATCTCTCAAGAAGAAATCATGTCGCCAAGACGAGTGGCCAC 66
OY 587 actctaactgaagaagcagaglatuaaagaacactagaacatcccttlttaacatccttga 646
DB 67 ACACCTACCGAGAACCGCTCCGACAGACTCCAGCACCCTTCTCACAGCCCTGAAG 126
OY 647 tattccttcagaagaagaacogtltgttltgtgtatgtgaatatttaagtgaggcgag 706
DB 127 TACTCTTTCACAGACCCAGCAGCCCTCTCTTTGTATGAGTACCCCAACGGGGCGAG 186
OY 707 ctgttttccattgtcggagagagcggtgtcttcgagagccgacacggtttcattgt 766
DB 187 CGTGTTTTCACCTGTCCCGGAGAGCGTGTCTTCGAGAGACCGGGCCGCTTATGGC 246
OY 767 ggaagaattgtctcgtccttgagactatcatctcgaaga--tltgtacggtat 823
DB 247 GCTGAGATGTGTGACCCCTGAGCTACCTGCACTCGAAGAAGAACTGTGTAACCGGAC 306
OY 824 ctcaagttggagatctaattgtctggaagaagatgagccacataaataatcacgatttga 883
DB 307 CTCGAAGCTGGAGAACTCATGTGTGACAGGAGCGGACACATTAAATCAACAACCTTCG 366
OY 884 ctctggaagaagagatcacagatgagacacatlaaagaacattctgtgtacactccaaga 943
DB 367 CTGTGCAAGAGAGGATCAAGAGAGCGTGCACCATTAAGACCTTTTGGCGCACACTTGA 426

FEATURES	SOURCE
1. 952	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone_image="IMAGE:4844129"	
/clone_id="NIH_MGC_43"	
/lab_type="normal pigmented retinal epithelium"	
/db_host="DH10B (phage-resistant)"	
/note="Organ: eye; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."	
Note: this is a NIH_MGC library."	
1004	ctagagggtctcatgatgaatgatgtgttggaaggtcttacctctctcaacacaggaacat 1063
1064	gagaaaccttttgaaataataataatgaagaaacataaattctctcgaaacctcttca 1123
547	GAGAAAGCTTTTGGAGCTCATCCTCATGAGAGAGATCCGCTTCCGCGACAGCTTGGTCCC 606
1124	gatcacaataatcattgcttccagggctcttgaaagga-tccaaataaacgcttggtg 1182
607	GAGGCCAAGTCTCTTCTTTCAGGGCTGCTCAAGAAAGAACCCCAAGACAGAGGCTTGGCGG 666
1183	aggaccagatgatgcacaagaatattatgagacacagttctctctctgtgaaactgtgca 1242
667	GGGCTCCGAGAGACCGCAAGAGATCATGACACATCGTTCTTTCGGGTATCCGTTGGG 726
1243	ag---atgatataataaaagctcttgacctctctttaaactcaag--taacatctgag 1297
727	AGCAGCTTTACGAGAAAGACGTCACGCCACCTTCAAGGCCACGAGGTCAACCTCGAG 786
1298	acagatactagatatatttga--tgaagaatttaccgtcagactacatacaataa 1349
787	ACTGACACACAGTATTTTGGACTCGAGAGAGTTACAGGGCCAGATGATACCATTA 840
RESULT 13	
LOCUS	BG749524
DEFINITION	BG749524 952 bp mRNA EST 15-MAY-2001
ACCESSION	BG749524
VERSION	BG749524.1 GI:14060177
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 952)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LNCM1681 row: d column: 18 High quality sequence stop: 766. location/Qualifiers

BASE COUNT	223 a	275 c	305 g	149 t	
ORIGIN					
Query Match	25.2%; Score 390.2; DB 11; Length 952;				
Best Local Similarity	71.6%; Pred. NO. 4.5e-85;				
Matches 569; Conservative	0; Mismatches 218; Indels 8; Gaps				
QY	ctgttatagagaagaacatttcattgtatagatactccagaggaagaagaatgtgacgaag 311				
DB	2 CTGTGATCGAAGCGACCTTCTCATGTGGAGACTCTGAGAGAGGGAGGAGGCAACCG 61				
QY	ctctcagagcgttgtagcgcagacaacctgcagagccaagaagaagaagaatgtgtagtc 371				
DB	62 CCATCTCAGACTGTGCGCTGAGCGGCTTCAAAAGCAGAGAGAGGAGAGTGTGACTTCCGCT 121				
QY	372 caacttcacaatltgataataatagagagaagaagatgtgtagtcctctcaaccatc--- 428				
DB	122 CGGGCTCACCCAGCAAGCAACTCAGGGGCTGAAGAGATGGAGTGTCCTCGGCCAAGGCCA 181				
QY	429 ataaagaagaagaacaatgtgatttgaactattgaaactactagtaagaagcactttg 488				
DB	182 AGCACCGCGTGACCATTGAAGACTTTGTGACTTACTTAAGCTGCTGGCGGCAAGGCACTTTCG 241				
QY	489 ggaagaattatttgggttcagagagaagaagcagcggaaataactatgactgtgaaatttga 548				
DB	242 GCAAGGTGATCTCGGTGTAAGAGAAAGGCCACAGGCCCTTACTACGCCCTTGAAGATCTCA 301				
QY	549 agaaagaagtcattatltgcacaagaagatgtgcacacacttaactgaagcagaagtat 608				
DB	302 AGAAGGAAGTATGTGTGGCCAAAGAGAGAGTGGCCCAACACTCAACGAGAAACGGGCTCC 361				
QY	609 taaagaacactagacatccctttaaacatccttgaatatccttccctcagaacaagaagc 668				
DB	362 TGCAGAACTCCAGGCAACCCCTTCTCACAGCCCTGAAGTACTCTTCCAGACCCACGACC 421				
QY	669 gtttggttttggatgtgaaatgtgttaatgtggg--gcagagcgtgttttccatttggaga 727				
DB	422 GCCTCTGCTTGTGATGTAGTATGACGCCAAGGGGTGAGACTGTTCTTCACCTGTCCGG 481				
QY	728 gagcgggctgtctctcgtgagacgcagacagcttctcactgtgcagaatgtgtctgcactg 787				
DB	482 GAGCGTGTGTCTCCAGAGGACCGGGCCGCTTCTATGGCGGTGAGATGTGTACAGCCCTG 541				
QY	788 gactatctaacatcgcgaaaga---ttgtgtaccggtgatctcaagtgtgagaatctaatg 844				
DB	542 GACTACTCTGCACCTCGGAGAAAGACGTGTGTACCGGGACCTCAACCTGGAACACTCATG 601				
QY	845 ctggaacaagaatgtgcacataaaaatttaagaatttgaacttggtaagaagaaggatataca 904				
DB	602 CTGGACAAGGACGGGCACTTAAAGTACACAGACTTGGGCTGTGCAAGAGAGGATCAAC 661				
QY	905 gatcagaccacactgaagaacatctgtgtgcactccaagaatctgtgcacagaggttcta 964				
DB	662 GACGGTGCACACATGAAGACCTTTTTCGGGCACACCTGATACCTTGCCCCGAGGTGCTG 721				
QY	965 gaagataatgactatgtgcagcagatagactgtgtgtgtgcctagtgaggttltcatgtgaa 1024				
DB	722 GAGGACATGTACTACGGGGCTGACGATGTGAGACTGTGTGGG--CTGGGGGTGTGATGTACGAC 780				
QY	1025 atgattgtgtgtggagg 1039				
DB	781 CTGATGTGACGAGACG 795				
RESULT 14					
LOCUS	BG747687 786 bp mRNA				
DEFINITION	602705158F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4841799 5'				
ACCESSION	BG747687				
VERSION	BG747687.1 GI:14058340				
KEYWORDS	EST.				

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SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 786)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L16M1675 row: c column: 16
            High quality sequence stop: 760.
            Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone="IMAGE:4841799"
                /clone_lib="NIH-MGC 43"
                /tissue_type="normal pigmented retinal epithelium"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: eye; Vector: pOTB1; Site: 1: XhoI; Site: 2:
                EcoRI; CDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(S). Library constructed by Ling Hong
                in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-CDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH-MGC Library."

BASE COUNT  177 a      219 c      253 g      137 t
ORIGIN

Query Match      24.9%; Score 385; DB 11; Length 786;
Best Local Similarity 71.6%; Pred. No. 8, 1e-84;
Matches 562; Conservative 0; Mismatches 215; Indels 8; Gaps 4;

OY  252 cgttatagagagaacattcatgtatagatccacagagagaagaagaatgagcgaag 311
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DB  2  cgtcatcgaaagcacccttcacatgctgagacatcttgagagcggcgagtgacacacg 61
OY  312 ctatccagcgttagacagacagactgcagagagaagaagaagaagaatgagcgaag 371
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  62  ccattccagactgtgctgacggcgcctcacaagacagagagagatgagcgaagcgg 121
OY  372 caacttcacaaatgataatagagagagaagaatgagcgaagcgaagcgaagcgaagc 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  122 cgggctcaccacccagctgacacacacacacacacacacacacacacacacacacac 181
OY  429 ataaaagaagaagaagaatgagcgaagcgaagcgaagcgaagcgaagcgaagcgaagc 488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  182 aacacccgctgacacacacacacacacacacacacacacacacacacacacacacac 241
OY  489 ggaagaatatttgctgagagaagaagaagaagaagaagaagaagaagaagaagaagaaga 548
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  242 gcaagtgatctctgctgagagagagagagagagagagagagagagagagagagagag 301
OY  549 aagaagaagtcattatgcaagaagatgagcagacacacacacacacacacacacacacac 608
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DB  302 aagaagaagtcattatgcaagaagatgagcagacacacacacacacacacacacacacac 361
OY  609 taagaagacactagacatcccttttaacatccttggaataatccttcacagacaaagacc 668
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DB  362 tgcagaaatccagagcacccttcctcagacagccctgaagaaatccttcacagacaaagacc 421
OY  669 gtttggttttgatgatgatgatgttaaggggagcagctgtttccatttgtagagag 728
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FEATURES
source

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DB  422 GCCTGTGCTTTGTGCATGAGTACGACCAAGGGGGGCGAGCTGTTCTTCCACTGCCCCGG 481
OY  729 aggggtgtttcttgagagccgacacagtttctatgtgcagaatgtgtcctgttg 788
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DB  482 AGCGTGTGTTCTCCGAGAGACCGGGCCCGCTCTATGCGCGTGTGATTTGTACGCCCTGG 541
OY  789 actatctacatcccggaagaaga---ttgttaccgtgatctcaagttggaagatctaagc 845
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DB  542 ACTACTGCACTGTGGAGAGAACGCTGTGTACCGGGACCTCAAGCTGGAGAACCTTATGC 601
OY  846 tggacaagaatggtccacataaaataacacagatttggacttgcagaagaaggatcacag 905
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DB  602 TGACACAAGAGCGGGCACATTAGATCACAGACTTCGGGCTGTGCAGAGAGGGGATCAAG 661
OY  906 atgcagccacatgaaagaatctgtgtgcacccacagaataatctgcacagaaggtgtg 965
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DB  662 ACGGTCCACCATGAAGACCTTTTGGGGCACACCTGATACCACTGAGCCCGGAGCTCTGG 721
OY  966 aaga-taatgacactatgcccagagcagatgagctgt-ggggcctaggggttgcattatga 1023
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DB  722 AGGACCAATGACTACGCGGCGTGCATGTGACTGTGGGGGGCTGGCGTGTATGACGA 781
OY  1024 aatga 1028
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DB  782 GATGA 786

RESULT  15
AA530983      387 bp      mRNA
n1j0h03.s1 NCI-CGAP Pr22 Homo sapiens CDNA clone IMAGE:985973 3'
similar to gb:M63167 RAC-ALPHA SERINE/THREONINE KINASE (HUMAN);,
mRNA sequence.
ACCESSION    AA530983
VERSION      AA530983.1 GI:2273689
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 387)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov.
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bhrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 385.
            Location/Qualifiers
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                /tissue_type="normal prostate"
                /lab_host="DH10B"
                /note="Organ: prostate; Vector: pRT30-Pac (Pharmacia)
                with a modified polylinker. 1st strand cDNA was prepared
                from normal prostate bulk tissue, and was then primed with
                a Not I - oligo(dT) primer. Double-stranded cDNA was
                ligated to Eco RI adaptors (Pharmacia), digested with Not
                I and cloned into the Not I and Eco RI sites of the
                modified pRT3 vector. Library is normalized, and was

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